James Acker :
Our next presenter is Radina Soebiyanto.

whose office shares a back wall with mine

Radina Soebiyanto:
Hi everyone

I will be talking about various works on modeling infectious diseases using environmental and climatological parameters from remote sensing and other sources, in which our group have done in the past years. Many of these diseases dynamics are associated with temperature, rainfall, land-use and so on. GIOVANNI has been an extremely useful resource to accomplish our work in public health application.

I will talk about 4 infectious diseases. For each disease I will first give a brief overview on the disease (such as the cause, burden, transmission pattern, etc), before going into the work we have done.

First is malaria.
About 35 countries contribute to 98% of global malaria deaths.
Women, children and anyone with depressed immunoresponse are at highest risk for malaria.
Current treatment and prevention include the use of artemisin-based combination therapy, bed nets, indoor spraying and vector control

The map here shows areas that are at risk of transmission.
Many of these countries are developing countries in tropical areas.
Climate change may lead to new areas that are suitable for the mosquitoes, and further cause outbreaks in previously unaffected regions.

The table on the right shows some of meteorological and environmental parameters that have been implicated in malaria.
Land-use type and altitude determines the vector habitat suitability.
The vector/mosquito life cycle, and it survivability, depends on the temperature and rainfall amount.

I think there is a problem with the table

It basically shows some of the environmental/climatolical determinants for malaria

James Acker :
Just a note, it appears tables in Powerpoint don't work well in WebEx.
We will have these presentations for examination after the workshop.

Radina Soebiyanto:
This is an example of malaria study in Thailand that our group has done.
Most of the endemic areas are near the borders where there are numbers of immigrants.
The pictures in the bottom show Mae La Camp, which is the largest refugee camp with more
than 30,000 populations. As you can see it is very dense.

This slide here shows the remote sensing data that we use to predict malaria cases in Thailand.
We have LST from MODIS, NDVI from AVHRR & MODIS, and Rainfall from TRMM.
For each of these variables, we showed the variability during Cool/Dry season (Nov-Jan),
Hot/Dry season (Feb-Apr), early rainy season (May-Jul) and late rainy season (Aug-Oct).

We use neural networks with the meteorological parameters as inputs, and the number
of malaria cases as the output. Our data was split into training and validation set.

Evidently as we increase the number of hidden nodes the training accuracy increases but the
prediction using validation data set decrease.
The graphs in the bottom left hand side show the accuracy for the training and validation
data set as the number of hidden nodes increase. These graphs are for 3 provinces indicated
in the map, which lies in the border.

Here are some graphs of all the predicted and the observed malaria cases for border
provinces using NDVI, LST and precipitation from TRMM.

We have also worked on using agent-based simulation to predict malaria cases in a village in Thailand.
The village is called Kong Mo Tha (KMT) village in the Kanchanaburi province.
This is an AFRIMS test site. Kong Mong Tha is an isolated village with about 700 people in a
narrow valley surrounded by high mountains.
It is only accessible by boats. There is not much in and out movement from the village

It is an ideal place for studying malaria transmission in a closed population.

Our collaborators at AFRIMS and Walter Reed have worked in this study site from nearly 5 years, collecting larval and blood samples.
The figures on the right hand side show the different habitat for different malarial mosquito species.

We used an agent-based, spatially explicit, discrete event simulation model. It models the detailed interactions among the vector life cycle, parasite sporogonic cycle, and human disease cycle under a whole set of intrinsic and extrinsic factors.
Assume we have an array of 5x5 houses except 2 houses are replaced by cattle sheds.
These are surrounded by 24 groups of larval habitats. Each habitat is not a single habitat, such as a single pool, but a group of pools – hence a composite habitat. The number of pools in the composite habitat can increase or decrease depending on rainfall.
Each household has 4 residents – one grandmother, one couple – husband and wife – and one child.
Each one has different social behavior and immunity.

These figures show the comparison of the simulations with the observations in 3 parameters:
Prevalence : % of infected humans
Sporozoite rate: % of infected mosquitoes
EIR (Entomological Inoculation Rate): # of infective bites a person received in a day

These are the simulations for 2000 days. Because malaria transmission is stochastic, the curves shown here are averaged from 100 simulations. This is driven by a sinusoidal supply of larval populations, reflecting the seasonal effects such as rainfall. The middle curve represents nominal mosquito loading, while the top and bottom show the higher and lower than nominal loading, respectively.

The bottom right-hand figure shows an example for hypothesis testing to simulate the effect of various control strategy. In this particular figure we show how cattle can be used to reduce malaria transmission effectively.

Now I will talk about how we use MODIS LST, TRMM and NDVI to project malaria cases in Afghanistan.
This work was done mainly by Farida Adimi and it has been published in Malaria journal.

About 60% of the Afghan population (~ 14 million) lives in malaria-endemic area.
414,407 malaria cases were reported in 2006, but WHO estimated that it could be as many as 600,000 cases per year.
Afghanistan's diverse landscape and terrain contributes to the heterogeneous malaria prevalence across the country. It is believed that malaria is endemic in areas below 2000 meters of elevation

and highly prevalent in river valleys where rice growing is common.

In this study we used regression technique to model malaria cases using inputs such as LST, TRMM and NDVI for 23 provinces in Afghanistan

The slides here show some of our results for a couple of the provinces.
We found that vegetation index, in general, is the strongest predictor. This reflected the fact that irrigation is the main factor that promotes malaria transmission in Afghanistan.

Surface temperature is the 2nd strongest predictor.
Precipitation is not a significant predictor, as it may not directly lead to higher larval population.

The malaria time series are modeled quite well, with provincial correlation average between the observed
and predicted malaria cases of about 0.845.

Sorry, this slide was not supposed to be here, because i thought it would take too much time to show our work for malaria in indonesia

I am actually going to show you our study on Dengue in Indonesia

Dengue is a tropical infectious disease. It is endemic in more than 110 countries, and primarily in the urban/peri urban areas.
It infects 50 – 100 million people, with 12,500 -25,000 deaths annually.
The burden is similar to other childhood and tropical diseases such as tuberculosis.
As a tropical disease, dengue is deemed 2nd in importance to malaria. WHO considers dengue as 1 of the 16 neglected tropical diseases.
Dengue symptoms are fever, headache, muscle and join pains, often called 'breakbone fever'.

Aedes mosquito is the primary vector that typically lives between 35N - 35S latitude and less than 1000 m elevation as shown in the map.
There are four types of the dengue pathogen virus. Most people typically recover from dengue without any problem. In some cases it leads to a more sever dengue, which is Dengue Hemorrhagic Fever,
and Dengue Shock. Any of the four serotypes can lead to this severe condition. One serotype may give lifelong immunity to that serotype but only short term to others. It is still not clear why secondary infection may lead to a more dangerous dengue.

We looked at dengue in Jakarta, the capital of Indonesia. In order to understand how meteorological factors are associated with dengue, we use a classical time series regression method, ARIMA, with external inputs including temperature, dew point, wind speed, TRMM and NDVI.

Our study showed that TRMM precipitation and dew point temperature are the best indicators for dengue incidences in Indonesia.

The graph on the right showed the observed and predicted dengue cases. As we could see that peak timing can be modeled accurately up to year 2004, but the accuracy decreased between year 2005 – 2006.

We were puzzled by this result. After talking to our collaborator in Indonesia, we found that vector control effort by the local government was started in the early 2005; hence the decreased number of dengue cases.

In the next couple slides I will talk about avian influenza study that we did in Indonesia.
Here is the background of Avian influenza

The figure her showed some of the outbreak around the world

This is some of the paths where avian influenza can be spread

We looked into avian influenza outbreaks in greater Jakarta area. We first did correlation and regression analysis between the outbreak and meteorological parameter such as temperature, rainfall from TRMM, dew point and wind speed. Neither poultry outbreak nor human cases show appreciable correlation with meteorological parameters

After that we looked into how far each of these outbreaks from roads, wet market, poultry distribution center, river and water body.

The histogram of the distance is shown in the figure.

We found that the risk for Avian Influenza outbreak in poultry is higher if it is less than 3 km from a wet market, or less than 500 meter from a river.

This result was consistent with the fact that Avian Influenza viruses survive well in water and can be transmitted through fomites (contaminated surfaces). As poultry vendors and consumers in Jakarta normally transport live and processed poultry in the open, it provides opportunity to

spread viruses around through fomites

The last topic is seasonal influenza.
This slide shows the burden of influenza and the spatiotemporal pattern of influenza circulation
in some countries.

In the temperate region, influenza is highest during winter time, however in the tropical regions
influenza is spread all year round. This observation is reflected in the top right-hand figure, which
shows influenza cases from the northern latitude in the US, down to Mexico, Columbia, Brazil and finally
Argentina in the southern hemisphere.

Several meteorological and socio-economic factors have been implicated in influenza. The most
common
ones are temperature and humidity which explain influenza peak during winter time in the temperate
regions. However, this is not applicable in many tropical regions.

Several countries in the tropics have observed a high influenza incidence that coincides with rainy
season such as in northeastern Brazil, Philippines and western part of India.

In this study we analyzed influenza transmission in Hong Kong (China), Maricopa County (Arizona, USA)
and New York City (New York, USA). This work has been published in PLoS ONE.

Both Hong Kong and Maricopa County have sub-tropical climate, whereas NYC has temperate climate.

We used influenza data retrieved from the associated public health agencies.

For meteorological data, we use precipitation from TRMM, LST from MODIS and ground station data
(such as temperature and humidity measures).

These data were aggregated into weekly to match the temporal resolution of the influenza
epidemiological data.

The bottom figures show TRMM, mean temperature and influenza laboratory-confirmed cases for each
region.

As you can see for Hong Kong, there are two peaks in each year. One is usually in early spring and
the other is in late summer.

In order to model weekly influenza cases, we used several techniques, including ARIMA and Neural Network.

These are some of the results from ARIMA and Neural Network. Inputs to these models include rainfall, dew point, mean temperature and solar radiation.

60 % of influenza variability in the US regions can be accounted by meteorological factors, whereas for Hong Kong the number of previous week cases is needed in the model. This suggests the role of contact transmission in Hong Kong.

That's all I have. Last but not least, all these work cannot be accomplished without the help of many of our collaborators listed here.

Thanks, Jim

James Acker:
Thank you, Radina, for an excellent presentation (we're learning about WebEx). I just sneezed, by the way!